

## SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> New nucleotide sequences which code for the menE gene

<130> 000551 BT

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<150> 4

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (230)..(1357)

<223> menE gene

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gtcaccaca atgggttgga actcaccggc gcaatcggcg ctggcgcgct gcttctcctc 120

30

gcagttggcg caggtgcatg gagcatcgac ggggttctgg caaacgcaa ggctaaatc 180

tagcgcaca actccgaatt ctgaaccatc ggcaactagaa tctcgggaat atg aat act 240

Met Asn Thr

35

1

cgc gtc ctc gaa gca cta cct gtt gat ctt gca gat ccc acc gca att 296

Arg Val Leu Glu Ala Leu Pro Val Asp Leu Ala Asp Pro Thr Ala Ile

5

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15

40

ctg gga gat ctc gag gac gca atc tct ggg aag aaa act ttc ctc ccc 354

Leu Gly Asp Leu Glu Asp Ala Ile Ser Gly Lys Lys Thr Phe Leu Pro

20

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45

atc cct gta caa gat aaa acc cgt gca cag ttg ctg cgc gat tct caa 380

Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg Asp Ser Gln

40

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50

cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc act 430

Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala Thr

55

60

65

55

tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg aat 478

Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu Asn

70

75

80

	ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa ggc	526
	Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu Gly	
	85 90 95	
5	cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag gtg	574
	Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln Val	
	100 105 110 115	
10	ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat ctc	622
	Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp Leu	
	120 125 130	
15	agc aca ggt ttt cac att gac gct ttc gca ggc gcc ggc gca gaa ctc	670
	Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu Leu	
	135 140 145	
20	aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag tta	718
	Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln Leu	
	150 155 160	
	ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctc aaa ctt ttt	766
	Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu Phe	
	165 170 175	
25	gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga att	814
	Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg Ile	
	180 185 190 195	
30	tct ggc gag cag cta gac atc aac att gtc acc acc tac ggc tcc tca	862
	Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser Ser	
	200 205 210	
35	gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc ggc	910
	Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly Ala	
	215 220 225	
40	aaa gtc cgt att tcc gat gag cgc att gag ttg ggt ggc cag atg att	958
	Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met Ile	
	230 235 240	
	ggc cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac gag	1006
	Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn Glu	
	245 250 255	
45	ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggc att ctc	1054
	Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile Leu	
	260 265 270 275	
50	acc gtg act ggt cgc gtg gat acc gtc att gat tcc ggt gga ttg aag	1102
	Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly Gly Leu Lys	
	280 285 290	
55	ttg cac cca gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc	1150
	Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val	
	295 300 305	
	acc ggc ggc tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca	1198
	Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala	
	310 315 320	

att gtg gcc gcg tac tcc gga tgg atc agt cgg tct gaa gtt att gaa 1246  
 Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu  
 325 330 335

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ggc ctc gac gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat 1294  
 Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His  
 340 345 350 355

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ctg gaa tct ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct 1342  
 Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala  
 360 365 370

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atc ggc aag ctg ttt tagtcttccat tcttgctggc tgcaactagt ttgcccacat 1397  
 Ile Ala Lys Leu Phe  
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attcattggg gtacactttg ggcattctgt catcatttcc acccatgagg gtgttgccaa 1457

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caactagtgc tcccacttgg gtggtgggca cgacagcgaa gtgtcggggc tgagcgtaga 1517  
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Phe Leu Pro Ile Pro Val Gln Asp Lys Thr Arg Ala Gln Leu Leu Arg  
 35 40 45

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Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val  
 50 55 60

Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr  
 65 70 75 80

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Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly  
 85 90 95

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Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly  
 100 105 110

Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala  
 115 120 125

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Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala  
 130 135 140

Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro  
 145 150 155 160

Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu  
165 170 175

5 Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln  
180 185 190

Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr  
195 200 205

10 Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile  
210 215 220

Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly  
15 225 230 235 240

Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe  
245 250 255

20 Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp  
260 265 270

Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Val Ile Asp Ser Gly  
275 280 285

25 Gly Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile  
290 295 300

Lys Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu  
305 310 315 320

Gly Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu  
325 330 335

35 Val Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg  
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Leu Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp  
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40 Arg Arg Ala Ile Ala Lys Leu Phe  
370 375

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•110• 3  
•111• 19  
•112• DNA  
•113• Corynebacterium glutamicum

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•120•  
•121• Primer menE-int1

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•400• 3  
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•111• 19

(1212) DNA

(1213) *Corynebacterium glutamicum*

(1220)

5 (1223) Primer menE-int2

(1400) 4

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